

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Degli-Esposti, Mariapia  
Goodwin, Raymond
- (ii) TITLE OF INVENTION: Novel Receptor That Causes Cell Death
- 10 (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Immunex  
(B) STREET: 51 University Street  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98101
- 20 (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: Apple Power Macintosh  
(C) OPERATING SYSTEM: Apple Operating System 7.5.3  
(D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
- 25 (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:  
(B) FILING DATE: 03 OCTOBER 1997  
(C) CLASSIFICATION:
- 30 (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: USSN 60/044,456  
(B) FILING DATE: 04 OCTOBER 1996  
(C) CLASSIFICATION:
- 35 (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Perkins, Patricia Anne  
(B) REGISTRATION NUMBER: 34,693  
(C) REFERENCE/DOCKET NUMBER: 2849-A
- 40 (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 2065870430
- 45 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1847 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: cDNA
- 55 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
- 60 (B) CLONE: AIR

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 236..1489

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTTTTCAGCC ATACCCGGAT GGTTCGTGCC TCGCTGGCCG TGATCACGCC GTCCTCCTTG 60

GGGATGAGCA GCGCGGCCGT GACGGCGTCC TGGTGCCCCCT CGATCTTGCT CAGCAGCACC 120

10 GGGCGGCTGC TCTGCGGCCT GGAGTGGATT TCGGCCGCCA TGTTGCGCGC GCGACTGCTG 180

CGGCCTCCTC GGCAGGCAGC CCATCAGCTG ACGCCTGGGC GCCCGTCGGA GGGCT ATG 238  
Met  
1

15 GAG CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC CTC CTG 286  
Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu Leu  
5 10 15

20 GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT CGT AGC CCC AGG TGT 334  
Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg Cys  
20 25 30

25 GAC TGT GCC GGT GAC TTC CAC AAG AAG ATT GGT CTG TTT TGT TGC AGA 382  
Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys Arg  
35 40 45

30 GGC TGC CCA GCG GGG CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC 430  
Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys  
50 55 60 65

35 GGC AAC TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC TGG 478  
Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala Trp  
70 75 80

40 GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG GCC TGT GAT GAG 526  
Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp Glu  
85 90 95

45 CAG GCC TCC CAG GTG GCG CTG GAG AAC TGT TCA GCA GTG GCC GAC ACC 574  
Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp Thr  
100 105 110

50 CGC TGT GGC TGT AAG CCA GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA 622  
Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser Gln  
115 120 125

55 TGT GTC AGC AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG 670  
Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly  
130 135 140 145

60 GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA GAT ACT GAC 718  
Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp  
150 155 160

65 TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA CAT GGC GAT GGC TGC GTG 766  
Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val  
165 170 175

70 TCC TGC CCC ACG AGC ACC CTG GGG AGC TGT CCA GAG CGC TGT GCC GCT 814  
Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala

	180					185					190						
5	GTC Val	TGT Cys 195	GGC Gly	TGG Trp	AGG Arg	CAG Gln	ATG Met 200	TTC Phe	TGG Trp	GTC Val	CAG Gln	GTG Val 205	CTC Leu	CTG Leu	GCT Ala	GGC Gly	862
10	CTT Leu 210	GTG Val	GTC Val	CCC Pro	CTC Leu	CTG Leu 215	CTT Leu	GGG Gly	GCC Ala	ACC Thr	CTG Leu 220	ACC Thr	TAC Tyr	ACA Thr	TAC Tyr	CGC Arg 225	910
15	CAC His	TGC Cys	TGG Trp	CCT Pro	CAC His 230	AAG Lys	CCC Pro	CTG Leu	GTT Val	ACT Thr 235	GCA Ala	GAT Asp	GAA Glu	GCT Ala	GGG Gly 240	ATG Met	958
20	GAG Glu	GCT Ala	CTG Leu	ACC Thr 245	CCA Pro	CCA Pro	CCG Pro	GCC Ala	ACC Thr 250	CAT His	CTG Leu	TCA Ser	CCC Pro	TTG Leu 255	GAC Asp	AGC Ser	1006
25	GCC Ala	CAC His	ACC Thr 260	CTT Leu	CTA Leu	GCA Ala	CCT Pro	CCT Pro	GAC Asp	AGC Ser	AGT Ser	GAG Glu	AAG Lys 270	ATC Ile	TGC Cys	ACC Thr	1054
30	GTC Val	CAG Gln 275	TTG Leu	GTG Val	GGT Gly	AAC Asn 280	AGC Ser	TGG Trp	ACC Thr	CCT Pro	GGC Gly	TAC Tyr 285	CCC Pro	GAG Glu	ACC Thr	CAG Gln	1102
35	GAG Glu 290	GCG Ala	CTC Leu	TGC Cys	CCG Pro	CAG Gln 295	GTG Val	ACA Thr	TGG Trp	TCC Ser	TGG Trp 300	GAC Asp	CAG Gln	TTG Leu	CCC Pro	AGC Ser 305	1150
40	AGA Arg	GCT Ala	CTT Leu	GGC Gly	CCC Pro 310	GCT Ala	GCT Ala	GCG Ala	CCC Pro	ACA Thr 315	CTC Leu	TCG Ser	CCA Pro	GAG Glu	TCC Ser 320	CCA Pro	1198
45	GCC Ala	GGC Gly	TCG Ser	CCA Pro 325	GCC Ala	ATG Met	ATG Met	CTG Leu	CAG Gln 330	CCG Pro	GGC Gly	CCG Pro	CAG Gln 335	CTC Leu	TAC Tyr	GAC Asp	1246
50	GTG Val	ATG Met	GAC Asp 340	GCG Ala	GTC Val	CCA Pro	GCG Ala	CGG Arg	CGC Arg	TGG Trp	AAG Lys	GAG Glu	TTC Phe 350	GTG Val	CGC Arg	ACG Thr	1294
55	CTG Leu	GGG Gly 355	CTG Leu	CGC Arg	GAG Glu	GCA Ala	GAG Glu 360	ATC Ile	GAA Glu	GCC Ala	GTG Val 365	GAG Glu	GTG Val	GAG Glu	ATC Ile	GGC Gly	1342
60	CGC Arg 370	TTC Phe	CGA Arg	GAC Asp	CAG Gln	CAG Gln 375	TAC Tyr	GAG Glu	ATG Met	CTC Leu	AAG Lys 380	CGC Arg	TGG Trp	CGC Arg	CAG Gln 385	CAG Gln	1390
65	CAG Gln	CCC Pro	GCG Ala	GGC Gly	CTC Leu 390	GGA Gly	GCC Ala	GTT Val	TAC Tyr	GCG Ala 395	GCC Ala	CTG Leu	GAG Glu	CGC Arg	ATG Met 400	GGG Gly	1438
70	CTG Leu	GAC Asp	GGC Gly	TGC Cys 405	GTG Val	GAA Glu	GAC Asp	TTG Leu	CGC Arg 410	AGC Ser	CGC Arg	CTG Leu	CAG Gln 415	CGC Arg	GGC Gly	CCG Pro	1486
75	TGA *	CACGGCGCCC	ACTTGCCACC	TAGGCGCTCT	GGTGGCCCTT	GCAGAAGCCC											1539

	TAAGTACGGT	TACTTATGCG	TGTAGACATT	TTATGTCACT	TATTAAGCCG	CTGGCACGGC	1599
	CCTGCGTAGC	AGCACCAGCC	GGCCCCACCC	CTGCTCGCCC	CTATCGCTCC	AGCCAAGGCG	1659
5	AAGAAGCACG	AACGAATGTC	GAGAGGGGGT	GAAGACATTT	CTCAACTTCT	CGGCCGGAGT	1719
	TTGGCTGAGA	TCGCGGTATT	AAATCTGTGA	AAGAAAACAA	AAAAAAAAAA	ACCGGAATTC	1779
	GATATCAAGC	TTATCGATAC	CGTCGACCTC	GAGGGGGGGC	CCGGTACCCA	ATTCGCCCTA	1839
10	TAGTGAGT						1847

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25	Met	Glu	Gln	Arg	Pro	Arg	Gly	Cys	Ala	Ala	Val	Ala	Ala	Ala	Leu	Leu
	1				5						10				15	
	Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser	Pro	Arg
				20					25					30		
30	Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu	Phe	Cys	Cys
			35					40					45			
	Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro	Cys	Thr	Glu	Pro
		50					55					60				
	Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln	Asp	Thr	Phe	Leu	Ala
	65					70					75					80
40	Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala	Arg	Cys	Gln	Ala	Cys	Asp
					85					90					95	
	Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu	Asn	Cys	Ser	Ala	Val	Ala	Asp
				100					105					110		
45	Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser
			115					120					125			
	Gln	Cys	Val	Ser	Ser	Ser	Pro	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys
		130					135					140				
	Gly	Ala	Leu	His	Arg	His	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr
						150					155					160
55	Asp	Cys	Gly	Thr	Cys	Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys
					165					170					175	
	Val	Ser	Cys	Pro	Thr	Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala
				180					185					190		
60	Ala	Val	Cys	Gly	Trp	Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala

	195	200	205
	Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr		
	210	215	220
5	Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly		
	225	230	235
10	Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp		
		245	250
	Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys		
		260	265
15	Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr		
		275	280
	Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro		
		290	295
20	Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser		
		305	310
	Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr		
		325	330
25	Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg		
		340	345
30	Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile		
		355	360
	Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln		
		370	375
35	Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met		
		385	390
	Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly		
		405	410
40	Pro *		

45 (2) INFORMATION FOR SEQ ID NO:3:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 55 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: FLAG® peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

60 Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

## (2) INFORMATION FOR SEQ ID NO:4:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 232 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Human

- 15 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: IgG1 Fc mutein

- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala  
 1 5 10 15  
 Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
 20 25 30  
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
 35 40 45  
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
 50 55 60  
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
 65 70 75 80  
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
 85 90 95  
 Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala  
 100 105 110  
 Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro  
 115 120 125  
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr  
 130 135 140  
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg  
 145 150 155 160  
 His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr  
 165 170 175  
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr  
 180 185 190  
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  
 195 200 205  
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys  
225 230

5

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 1251 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Murine AIR

25

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 7..1239

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

30

GTCGAC ATG GAG GCA CGG CTG CTG CGG GGC TGC GTG GTG GAG CCT CTG 48  
Met Glu Ala Arg Leu Leu Arg Gly Cys Val Val Glu Pro Leu  
1 5 10

35

TTC CTA CCA CTG CTG CTG CTG CTG CTG CTG CTT GGT GGC CAG GGC 96  
Phe Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu Gly Gly Gln Gly  
15 20 25 30

40

CAG GGC GGC ATG TCT GGC AGG TGT GAC TGT GCC AGT GAG TCC CAG AAG 144  
Gln Gly Gly Met Ser Gly Arg Cys Asp Cys Ala Ser Glu Ser Gln Lys  
35 40 45

45

AGG TAT GGC CCG TTT TGT TGC AGG GGC TGC CCA AAG GGA CAC TAC ATG 192  
Arg Tyr Gly Pro Phe Cys Cys Arg Gly Cys Pro Lys Gly His Tyr Met  
50 55 60

50

AAG GCC CCC TGC GCA GAA CCC TGT GGC AAC TCC ACC TGC CTT CCC TGT 240  
Lys Ala Pro Cys Ala Glu Pro Cys Gly Asn Ser Thr Cys Leu Pro Cys  
65 70 75

55

CCC TCG GAC ACC TTC TTG ACC AGA GAC AAC CAC TTT AAG ACT GAC TGT 288  
Pro Ser Asp Thr Phe Leu Thr Arg Asp Asn His Phe Lys Thr Asp Cys  
80 85 90

ACC CGC TGC CAA GTC TGT GAT GAA GAG GCC CTT CAA GTG ACC CTT GAG 336  
Thr Arg Cys Gln Val Cys Asp Glu Glu Ala Leu Gln Val Thr Leu Glu  
95 100 105 110

60

AAC TGC TCG GCA AAG TCG GAC ACC CAC TGT GGC TGC CAG TCA GGC TGG 384  
Asn Cys Ser Ala Lys Ser Asp Thr His Cys Gly Cys Gln Ser Gly Trp  
115 120 125

	TGT	GTT	GAC	TGC	TCC	ACC	GAG	CCA	TGT	GGG	AAA	AGC	TCA	CCT	TTC	TCT	432
	Cys	Val	Asp	Cys	Ser	Thr	Glu	Pro	Cys	Gly	Lys	Ser	Ser	Pro	Phe	Ser	
				130					135					140			
5	TGT	GTC	CCA	TGC	GGG	GCT	ACA	ACA	CCA	GTC	CAT	GAG	GCT	CCA	ACC	CCC	480
	Cys	Val	Pro	Cys	Gly	Ala	Thr	Thr	Pro	Val	His	Glu	Ala	Pro	Thr	Pro	
			145					150					155				
10	CGG	CCC	TGC	CTG	CCT	GGC	TTC	TAT	ATA	CGT	GGC	AAT	GAC	TGC	ACG	TCC	528
	Arg	Pro	Cys	Leu	Pro	Gly	Phe	Tyr	Ile	Arg	Gly	Asn	Asp	Cys	Thr	Ser	
		160					165					170					
15	TGC	CCC	ACG	GGC	TTC	AGC	AGC	GTT	TGC	CCT	AAG	GCT	TGC	ACT	GCT	GTC	576
	Cys	Pro	Thr	Gly	Phe	Ser	Ser	Val	Cys	Pro	Lys	Ala	Cys	Thr	Ala	Val	
	175					180					185					190	
20	TGT	GGC	TGG	AAG	CAG	ATG	TTT	TGG	GTC	CAG	GTG	CTT	CTA	GGA	GTC	GCG	624
	Cys	Gly	Trp	Lys	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Gly	Val	Ala	
					195				200						205		
25	TTC	CTT	TTT	GGG	GCT	ATC	CTG	ATC	TGT	GCA	TAT	TGT	CGA	TGG	CAG	CCT	672
	Phe	Leu	Phe	Gly	Ala	Ile	Leu	Ile	Cys	Ala	Tyr	Cys	Arg	Trp	Gln	Pro	
				210					215					220			
30	TGT	AAG	GCC	GTG	GTC	ACT	GCA	GAC	ACA	GCT	GGG	ACG	GAG	ACC	CTG	GCC	720
	Cys	Lys	Ala	Val	Val	Thr	Ala	Asp	Thr	Ala	Gly	Thr	Glu	Thr	Leu	Ala	
			225					230					235				
35	TCA	CCA	CAG	ACT	GCC	CAT	CTC	TCA	GCC	TCA	GAC	AGC	GCC	CAC	ACC	CTC	768
	Ser	Pro	Gln	Thr	Ala	His	Leu	Ser	Ala	Ser	Asp	Ser	Ala	His	Thr	Leu	
		240					245					250					
40	CTG	GCA	CCT	CCA	AGC	AGT	ACT	GGG	AAA	ATC	TGT	ACC	ACT	GTC	CAG	TTG	816
	Leu	Ala	Pro	Pro	Ser	Ser	Thr	Gly	Lys	Ile	Cys	Thr	Thr	Val	Gln	Leu	
	255					260					265					270	
45	GTA	GGC	AAC	AAC	TGG	ACC	CCT	GGC	TTA	TCC	CAG	ACT	CAG	GAG	GTG	GTC	864
	Val	Gly	Asn	Asn	Trp	Thr	Pro	Gly	Leu	Ser	Gln	Thr	Gln	Glu	Val	Val	
					275				280						285		
50	TGC	GGA	CAG	GCC	TCA	CAA	CCC	TGG	GAT	CAG	CTG	CCA	AAC	AGA	ACT	CTT	912
	Cys	Gly	Gln	Ala	Ser	Gln	Pro	Trp	Asp	Gln	Leu	Pro	Asn	Arg	Thr	Leu	
				290					295					300			
55	GGA	ACT	CCT	CTG	GCA	TCT	CCG	CTC	TCG	CCA	GCG	CCC	CCT	GCG	GGC	TCT	960
	Gly	Thr	Pro	Leu	Ala	Ser	Pro	Leu	Ser	Pro	Ala	Pro	Pro	Ala	Gly	Ser	
			305					310					315				
60	CCG	GCT	GCT	GTG	CTC	CAG	CCT	GGC	CCG	CAG	CTC	TAC	GAT	GTG	ATG	GAT	1008
	Pro	Ala	Ala	Val	Leu	Gln	Pro	Gly	Pro	Gln	Leu	Tyr	Asp	Val	Met	Asp	
		320					325					330					
65	GCG	GTC	CCA	GCA	CGA	AGG	TGG	AAG	GAG	TTC	GTG	CGC	ACG	CTG	GGG	CTG	1056
	Ala	Val	Pro	Ala	Arg	Arg	Trp	Lys	Glu	Phe	Val	Arg	Thr	Leu	Gly	Leu	
	335					340					345					350	
70	CGG	GAA	GCG	GAA	ATT	GAA	GCC	GTG	GAG	GTG	GAA	ATC	TGC	CGC	TTC	CGA	1104
	Arg	Glu	Ala	Glu	Ile	Glu	Ala	Val	Glu	Val	Glu	Ile	Cys	Arg	Phe	Arg	
					355					360					365		
75	GAC	CAG	CAG	TAT	GAG	ATG	CTC	AAG	CGC	TGG	CGT	CAG	CAG	CAG	CCT	GCA	1152



Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala  
 370 375 380

5 GGC CTC GGT GCC ATC TAT GCG GCT CTG GAG CGC ATG GGT CTG GAA GGC 1200  
 Gly Leu Gly Ala Ile Tyr Ala Ala Leu Glu Arg Met Gly Leu Glu Gly  
 385 390 395

10 TGT GCC GAG GAC CTG CGC AGC CGC CTG CAG CGT GGC CCG TGATGCGGCC 1249  
 Cys Ala Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro  
 400 405 410

GC 1251

15 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25 Met Glu Ala Arg Leu Leu Arg Gly Cys Val Val Glu Pro Leu Phe Leu  
 1 5 10 15

30 Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu Gly Gly Gln Gly Gln Gly  
 20 25 30

Gly Met Ser Gly Arg Cys Asp Cys Ala Ser Glu Ser Gln Lys Arg Tyr  
 35 40 45

35 Gly Pro Phe Cys Cys Arg Gly Cys Pro Lys Gly His Tyr Met Lys Ala  
 50 55 60

Pro Cys Ala Glu Pro Cys Gly Asn Ser Thr Cys Leu Pro Cys Pro Ser  
 65 70 75 80

40 Asp Thr Phe Leu Thr Arg Asp Asn His Phe Lys Thr Asp Cys Thr Arg  
 85 90 95

45 Cys Gln Val Cys Asp Glu Glu Ala Leu Gln Val Thr Leu Glu Asn Cys  
 100 105 110

Ser Ala Lys Ser Asp Thr His Cys Gly Cys Gln Ser Gly Trp Cys Val  
 115 120 125

50 Asp Cys Ser Thr Glu Pro Cys Gly Lys Ser Ser Pro Phe Ser Cys Val  
 130 135 140

Pro Cys Gly Ala Thr Thr Pro Val His Glu Ala Pro Thr Pro Arg Pro  
 145 150 155 160

55 Cys Leu Pro Gly Phe Tyr Ile Arg Gly Asn Asp Cys Thr Ser Cys Pro  
 165 170 175

60 Thr Gly Phe Ser Ser Val Cys Pro Lys Ala Cys Thr Ala Val Cys Gly  
 180 185 190

	Trp	Lys	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Gly	Val	Ala	Phe	Leu	
			195					200					205				
5	Phe	Gly	Ala	Ile	Leu	Ile	Cys	Ala	Tyr	Cys	Arg	Trp	Gln	Pro	Cys	Lys	
		210					215					220					
	Ala	Val	Val	Thr	Ala	Asp	Thr	Ala	Gly	Thr	Glu	Thr	Leu	Ala	Ser	Pro	
	225					230					235					240	
10	Gln	Thr	Ala	His	Leu	Ser	Ala	Ser	Asp	Ser	Ala	His	Thr	Leu	Leu	Ala	
					245					250					255		
	Pro	Pro	Ser	Ser	Thr	Gly	Lys	Ile	Cys	Thr	Thr	Val	Gln	Leu	Val	Gly	
				260					265					270			
15	Asn	Asn	Trp	Thr	Pro	Gly	Leu	Ser	Gln	Thr	Gln	Glu	Val	Val	Cys	Gly	
			275					280					285				
	Gln	Ala	Ser	Gln	Pro	Trp	Asp	Gln	Leu	Pro	Asn	Arg	Thr	Leu	Gly	Thr	
20		290					295					300					
	Pro	Leu	Ala	Ser	Pro	Leu	Ser	Pro	Ala	Pro	Pro	Ala	Gly	Ser	Pro	Ala	
	305					310					315					320	
25	Ala	Val	Leu	Gln	Pro	Gly	Pro	Gln	Leu	Tyr	Asp	Val	Met	Asp	Ala	Val	
					325					330					335		
	Pro	Ala	Arg	Arg	Trp	Lys	Glu	Phe	Val	Arg	Thr	Leu	Gly	Leu	Arg	Glu	
				340					345					350			
30	Ala	Glu	Ile	Glu	Ala	Val	Glu	Val	Glu	Ile	Cys	Arg	Phe	Arg	Asp	Gln	
			355				360						365				
	Gln	Tyr	Glu	Met	Leu	Lys	Arg	Trp	Arg	Gln	Gln	Gln	Pro	Ala	Gly	Leu	
35		370					375					380					
	Gly	Ala	Ile	Tyr	Ala	Ala	Leu	Glu	Arg	Met	Gly	Leu	Glu	Gly	Cys	Ala	
	385				390						395					400	
40	Glu	Asp	Leu	Arg	Ser	Arg	Leu	Gln	Arg	Gly	Pro						
					405					410							